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OM nucleic - nucleic search, using sw model

Run on: August 28, 2006, 09:45:23 ; Search time 150 Seconds
(without alignments)
424.118 Million cell updates/sec

Title: US-09-847-601B-100
Sequence: 1 ucgaacugaugagccgucgscgaacgaag 34

Scoring table: OLIGO_NIC
Gapop 60.0, Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: Issued Patents NA:*
- 2: /EMC_Celerra_SIDS3/prodata/2/ina/1 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/prodata/2/ina/5 COMB.seq:*
- 4: /EMC_Celerra_SIDS3/prodata/2/ina/6A COMB.seq:*
- 5: /EMC_Celerra_SIDS3/prodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/prodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SIDS3/prodata/2/ina/PP COMB.seq:*
- 8: /EMC_Celerra_SIDS3/prodata/2/ina/RE COMB.seq:*
- 9: /EMC_Celerra_SIDS3/prodata/2/ina/Backfile1.seq:*
- 10: /EMC_Celerra_SIDS3/prodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	34	100.0	34	US-09-874-601-100	Sequence 100, App
2	27	79.4	32	US-09-874-601-101	Sequence 101, App
3	27	79.4	34	US-09-874-601-98	Sequence 98, Appl
4	26	76.5	34	US-09-874-601-92	Sequence 92, Appl
5	26	76.5	34	US-09-874-601-93	Sequence 93, Appl
6	26	76.5	34	US-09-874-601-99	Sequence 99, Appl
7	25	73.5	34	US-09-874-601-90	Sequence 90, Appl
8	25	73.5	34	US-09-874-601-91	Sequence 91, Appl
9	25	73.5	34	US-09-874-601-95	Sequence 95, Appl
10	25	73.5	34	US-09-874-601-96	Sequence 96, Appl
11	25	73.5	34	US-09-874-601-97	Sequence 97, Appl
12	19	55.9	34	US-09-874-601-94	Sequence 94, Appl
13	15	44.1	333	US-09-489-039A-3537	Sequence 3537, Ap
14	15	44.1	601	US-09-949-016-81813	Sequence 81813, A
15	15	44.1	1152	US-09-045-186-1	Sequence 1, Appl
16	15	44.1	1152	US-09-045-186-3	Sequence 3, Appl
17	15	44.1	1338	PCT-US93-05039-2	Sequence 2, Appl
18	15	44.1	1534	PCT-US93-05039-1	Sequence 1, Appl
19	15	44.1	1605	US-09-676-970-1	Sequence 1, Appl
20	15	44.1	1605	US-09-676-972B-1	Sequence 1, Appl
21	15	44.1	1605	US-09-016-434-1231	Sequence 1231, Ap
22	15	44.1	1605	US-09-676-941A-1	Sequence 1, Appl
23	15	44.1	1605	US-10-013-846-3	Sequence 3, Appl

24	15	44.1	1605	3	US-10-291-446-1	Sequence 1, Appl
25	15	44.1	1605	3	US-10-410-648-3	Sequence 3, Appl
26	15	44.1	1605	5	US-10-274-851-3	Sequence 3, Appl
27	15	44.1	1605	3	US-09-370-767-11487	Sequence 11487, A
28	15	44.1	2624	2	US-08-232-144-3	Sequence 3, Appl
29	15	44.1	2624	3	US-09-708-392-10	Sequence 10, Appl
30	15	44.1	4571	2	US-08-232-144-5	Sequence 5, Appl
31	15	44.1	12001	2	US-08-458-568A-11	Sequence 11, Appl
32	15	44.1	125192	3	US-09-949-016-14120	Sequence 14120, A
33	15	44.1	125192	3	US-09-949-016-13860	Sequence 13860, A
34	15	44.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl
35	15	44.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl
36	15	41.2	36	2	US-08-334-847-806	Sequence 806, App
37	14	41.2	38	3	US-09-371-772B-11589	Sequence 11589, A
38	14	41.2	38	3	US-09-371-772B-11932	Sequence 11932, A
39	14	41.2	38	5	US-10-138-674B-11865	Sequence 11865, A
40	14	41.2	38	5	US-10-138-674B-14209	Sequence 14209, A
41	14	41.2	491	3	US-09-640-211A-529	Sequence 529, App
42	14	41.2	498	3	US-09-302-540-8002	Sequence 8002, Ap
43	14	41.2	570	3	US-09-328-352-2408	Sequence 2408, Ap
44	14	41.2	601	3	US-09-949-016-121350	Sequence 121350, A
45	14	41.2	601	3	US-09-533-559-3649	Sequence 3649, Ap

ALIGNMENTS

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RESULT 1
US-09-874-601-100
; Sequence 100, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 100
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-100
Query Match      100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy      1 UGCAACTGUGAGCGGUCGCGGCAACGAAG 34
Db      1 UGCAACTGUGAGCGGUCGCGGCAACGAAG 34
RESULT 2
US-09-874-601-101
; Sequence 101, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.

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; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-101
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Query Match          79.4%; Score 27; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      5 AACUGAUGAGCCGUCGCGGCGGAACG 31
      |||
Db      3 AACUGAUGAGCCGUCGCGGCGGAACG 29
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RESULT 3
US-09-874-601-98
; Sequence 98, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-98
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Query Match          79.4%; Score 27; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      5 AACUGAUGAGCCGUCGCGGCGGAACG 31
      |||
Db      5 AACUGAUGAGCCGUCGCGGCGGAACG 31
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RESULT 4
US-09-874-601-92
; Sequence 92, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-92
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Query Match          76.5%; Score 26; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      5 AACUGAUGAGCCGUCGCGGCGGAAC 30
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Db      5 AACUGAUGAGCCGUCGCGGCGGAAC 30
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RESULT 5
US-09-874-601-93
; Sequence 93, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 93
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-93
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Query Match          76.5%; Score 26; DB 3; Length 34;
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Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAGCGCGUCCGGCGGAAC 30
Db 5 AACUGAGCGCGUCCGGCGGAAC 30

RESULT 6

US-09-874-601-99
; Sequence 99, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 99
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-99

Query Match 76.5%; Score 26; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAGCGCGUCCGGCGGAAC 30
Db 5 AACUGAGCGCGUCCGGCGGAAC 30

RESULT 7

US-09-874-601-90
; Sequence 90, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 90
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-90

Query Match 73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACUGAUGAGCGCGUCCGGCGGAAC 30
Db 6 ACUGAUGAGCGCGUCCGGCGGAAC 30

RESULT 8

US-09-874-601-91
; Sequence 91, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 91
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-91

Query Match 73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACUGAUGAGCGCGUCCGGCGGAAC 30
Db 6 ACUGAUGAGCGCGUCCGGCGGAAC 30

RESULT 9

US-09-874-601-95
; Sequence 95, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492

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; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-95

Query Match      73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACUGAUGAGCGGUCGCGCGGAAC 30
DB      6 ACUGAUGAGCGGUCGCGCGGAAC 30

RESULT 10
US-09-874-601-96
; Sequence 96, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-96

Query Match      73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACUGAUGAGCGGUCGCGCGGAAC 30
DB      6 ACUGAUGAGCGGUCGCGCGGAAC 30

RESULT 11
US-09-874-601-97
; Sequence 97, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
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; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 97
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-97

Query Match      73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACUGAUGAGCGGUCGCGCGGAAC 30
DB      6 ACUGAUGAGCGGUCGCGCGGAAC 30

RESULT 12
US-09-874-601-94
; Sequence 94, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 94
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-94

Query Match      55.9%; Score 19; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GAGCGGUCGCGCGGAAC 30
DB      12 GAGCGGUCGCGCGGAAC 30

RESULT 13
US-09-489-039A-3537/C
; Sequence 3537, Application US/09489039A
; Patent No. 6610836
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; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3537
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-3537

Query Match      44.1%; Score 15; DB 3; Length 333;
Best Local Similarity 86.7%; Pred. No. 26;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      15 CCGTTCGGCGGCGGAAA 29
DB      62 CCGTTCGGCGGCGGAAA 48

RESULT 14
US-09-949-016--81813
; Sequence 81813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81813
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016--81813

Query Match      44.1%; Score 15; DB 3; Length 601;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 UGCAACUGAGGAGC 15
DB      41 TGCAACTGATGAGC 55

RESULT 15
US-09-045-186-1
; Sequence 1, Application US/09045186
; Patent No. 6087154
; GENERAL INFORMATION:
; APPLICANT: Baez, Melvyn
; APPLICANT: Cates, Carolyn A.
; TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
```

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; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,186
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: P-11376
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1152
; US-09-045-186-1

Query Match      44.1%; Score 15; DB 3; Length 1152;
Best Local Similarity 73.3%; Pred. No. 26;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACTGAGAGCGCGGTC 20
DB      538 ACTGATGAGCGGTC 552
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Search completed: August 28, 2006, 10:29:28
Job time : 154 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 28, 2006, 09:45:12 ; Search time 285 Seconds
(without alignments)
831.777 Million cell updates/sec

Title: US-09-847-601B-100

Sequence: 1 ugcaaacugaugagccgguucgcgcggaacgaag 34

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

Database : N_GeneSeq_8: *

- 1: _ geneeqn1980s: *
2: geneeqn1990s: *
3: geneeqn2000s: *
4: geneeqn2001as: *
5: geneeqn2001bs: *
6: geneeqn2002as: *
7: geneeqn2002bs: *
8: geneeqn2003as: *
9: geneeqn2003bs: *
10: geneeqn2003cs: *
11: geneeqn2003ds: *
12: geneeqn2004as: *
13: geneeqn2004bs: *
14: geneeqn2005s: *
15: geneeqn2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	34	100.0		34	10	AB272865	Ab272865 IGf1 R21
	2	27	79.4		32	10	AB272866	Ab272866 IGf1 R22
	3	27	79.4		34	10	AB272863	Ab272863 Alpha V
	4	26	76.5		34	10	AB272867	Ab272867 Alpha 3
	5	26	76.5		34	10	AB272868	Ab272868 Alpha 3
	6	26	76.5		34	10	AB272873	Ab272873 VEGFR2 R
	7	26	76.5		34	10	AB272864	Ab272864 Alpha V
	8	25	76.5		34	10	AB272872	Ab272872 VEGFR2 R
	9	25	73.5		34	10	AB272875	Ab272875 A2B R21
	10	25	73.5		34	10	AB272862	Ab272862 Alpha 1
	11	25	73.5		34	10	AB272856	Ab272856 A2B R22
	12	25	73.5		34	10	AB272870	Ab272870 VEGFR1 R
	13	25	73.5		34	10	AB272860	Ab272860 Alpha 5
	14	25	73.5		44	3	AB272861	Ab272861 Alpha 1
	15	25	73.5		44	3	AA288594	AA288594 Oligonucleotide
	16	24	70.6		34	3	AA288555	AA288555 Anti-SOD
	17	24	70.6		34	3	AA288557	AA288557 Anti-SOD
	18	24	70.6		34	3	AA288559	AA288559 Anti-SOD

19	24	70.6	34	3	AAc88561	Anti-SOD-
20	24	70.6	34	10	ABc72871	ABc72871 VEGF1 R
21	24	70.6	35	3	AAc88537	AAc88537 Anti-gamm
22	24	70.6	35	3	AAc88535	AAc88535 Anti-gamm
23	24	70.6	36	3	AAc88559	AAc88559 Oligonuc
24	24	70.6	36	3	AAc88557	AAc88557 Oligonuc
25	24	70.6	36	3	AAc88553	AAc88553 Oligonuc
26	24	70.6	44	3	AAc88558	AAc88558 Oligonuc
27	24	70.6	44	3	AAc88556	AAc88556 Oligonuc
28	24	70.6	44	3	AAc88552	AAc88552 Oligonuc
29	19	55.9	34	10	ABc72859	ABc72859 Alpha 5 I
30	16	47.1	456	15	AAcF82077	AAcF82077 Human S
31	16	47.1	564	15	AAcF16550	AAcF16550 Nocardi
32	16	47.1	564	15	AAcF16552	AAcF16552 Nocardi
33	16	47.1	564	15	AAcF16551	AAcF16551 Nocardi
34	16	47.1	1140	15	AAcF16575	AAcF16575 Alkaline
35	16	47.1	1143	15	AAcF16520	AAcF16520 Nocardi
36	16	47.1	1143	15	AAcF16522	AAcF16522 Nocardi
37	16	47.1	1143	15	AAcF16518	AAcF16518 Nocardi
38	16	47.1	1143	15	AAcF16578	AAcF16578 Alkaline
39	16	47.1	1143	15	AAcF16577	AAcF16577 Alkaline
40	16	47.1	1143	15	AAcF16579	AAcF16579 Alkaline
41	16	47.1	1482	8	ADA70476	ADA70476 Rice gene
42	16	47.1	1549	9	ADA48529	ADA48529 Rice gene
43	16	47.1	6949	10	ABc051485	ABc051485 Bacteria
44	16	47.1	6949	10	ABc055593	ABc055593 Drosophi
45	15	44.1	100	8	ACb80108	ACb80108 E. coli K

ALIGNMENTS

RESULT 1

ID ABZ72865 standard; RNA; 34 BP.

AC ABZ72865 ;

DT 09-APR-2003 (first entry)

DE IGF1 R21 exemplary ribozyme construct SEQ ID NO:100.

KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
 ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;

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PT useful for treating a disease or dysfunction of the mammalian eye e.g. retinitis pigmentosa or age related macular

pt degeneration.

PS Claim 1; Page 81; 115pp; English.

The

CC First ribozyme that specifically cleaves an mRNA encoding a protein,

CC polypeptide or peptide selected from the group of rod opsin, *inOS*,
CC RbG, peripherin, *VEGFR1*, *VEGFR2*, adenosine A-2B receptor, *IGF-1*, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC dysfunction, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autoimmune dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention

XX Sequence 34 BP, 10 A, 8 C, 11 G, 0 T, 5 U, 0 Other;

Query Match	100.0%	Score 34	DB 10	Length 34
Best Local Similarity	100.0%	Pred. NC	6.9e-09	
Matches 34	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy

1 UGCAAACTCAGUAGAAGCGGUUCGGCGGAACGAAG 34
Dd

1 UGCAAATCTAUGAGCCGCUUCGCCGCACAACGAAG 34

RESULT 2
ABZ72866
ID ABZ72866 standard; RNA; 32 BP.

AC ABZ72866;

DT 09-APR-2003 (first entry)

DE IGF1 R22 exemplary ribozyme construct SEQ ID NO:101.

kw Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

diabetic retinopathy; macular degeneration; autosomal dominant retinitis;

XX

OS Synthetic.

PN WO200288320-A2.

PD 07-NOV-2002

PF 01-MAY-2002; 2002WO-US013679.

PR 01-MAY-2001; 2001US-00847601.

PA (UYFL) UNIV FLORIDA.

PI Lewin AS, Shaw LC, Grant MB;

DR WPI; 2003-111880/10.

PT A recombinant adeno-associated virus-vectored ribozyme composition,

PT retinal disease, e.g. diabetic retinopathy or age-related macular

 χ^2

PS Claim 1; Page 81; 115pp; English.

The present invention describes recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, inosin, RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a vector comprising a polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal dysfunction, (diabetic) retinopathy, or (age-related) macular degeneration.. (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (I) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. AB272763 to AB272935 represent sequences used in the exemplification of the present invention

sq Sequence 32 BP; 8 A; 8 C; 11 G; 0 T; 5 U; 0 Other;

Query Match	79.4%	Score 27	DB 10	Length 32
Best Local Similarity	100.0%	Pred. No.	4.7e-05	
Matches 27	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 5 AACUGAUGAGCCGUTCGCGCGAAACG 31
|||
Db 3 AACUGAUGAGCCGUTCGCGCGAAACG 29

119

ABZ72863

XX

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XX 5

XX

KW Hai

KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;

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PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.

PS Claim 1, Page 80; 115pp; English.

CC The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, INOS,
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention

CC Sequence 34 BP; 7 A; 10 C; 13 G; 0 T; 4 U; 0 Other;

CC Query Match 79.4%; Score 27; DB 10; Length 34;

CC Best Local Similarity 100.0%; Pred. No. 4.7e-05; Mismatches 0; Indels 0; Gaps 0;

CC Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 5 AACUGAUGAGCCGCGCGGCGGAAACG 31

CC 5 AACUGAUGAGCCGCGGCGGCGGAAACG 31

CC AB272857;

CC 09-APR-2003 (first entry)

CC Alpha 3 R21 exemplary ribozyme construct SEQ ID NO:92.

CC Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
CC ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
CC diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
CC blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

CC Synthetic.

CC WO200288320-A2.

CC 07-NOV-2002.

CC 01-MAY-2002; 2002WO-US013679.

CC 01-MAY-2001; 2001US-00847601.

CC (UYFL) UNIV FLORIDA.

XX Lewin AS, Shaw LC, Grant MB;
XX WPI; 2003-111880/10.

XX A recombinant adeno-associated virus-vectored ribozyme composition,
XX useful for treating a disease or dysfunction of the mammalian eye e.g.
XX retinal disease, e.g. diabetic retinopathy or age-related macular
XX degeneration.

PS Claim 1, Page 80; 115pp; English.

CC The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, INOS,
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention

CC Sequence 34 BP; 10 A; 8 C; 10 G; 0 T; 6 U; 0 Other;

CC Query Match 76.5%; Score 26; DB 10; Length 34;

CC Best Local Similarity 100.0%; Pred. No. 0.00016; Mismatches 0; Indels 0; Gaps 0;

CC 5 AACUGAUGAGCCGCGCGGCGGAAAC 30

CC 5 AACUGAUGAGCCGCGGCGGCGGAAAC 30

CC AB272858

CC Alpha 3 R22 exemplary ribozyme construct SEQ ID NO:93.

CC Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
CC ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
CC diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
CC blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

CC Synthetic.

CC WO200288320-A2.

CC 07-NOV-2002.

CC 01-MAY-2001; 2001US-00847601.

CC (UYFL) UNIV FLORIDA.

PF 01-MAY-2002; 2002MO-US013679.
XX
PR 01-MAY-2001; 2001US-00847601.
XX
XX (UYFL) UNIV FLORIDA.
PA
XX Lewin AS, Shaw LC, Grant MB;
XX
DR WPI; 2003-111880/10.
XX
PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
XX
XX Claim 1; Page 80; 115pp; English.
XX
CC The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, INOS,
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC dysfunction, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC local vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 34 BP; 8 A; 8 C; 13 G; 0 T; 5 U; 0 Other;
XX
Query Match 76.5%; Score 26; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 AACUGAUGAGCCGUCGCGGGAAC 30
DB 5 AACUGAUGAGCCGUCGCGGGAAC 30
XX
RESULT 6
AB272873
ID AB272873 standard; RNA; 34 BP.
XX
AC AB272873;
XX
DT 09-APR-2003 (first entry)
XX
DE VEGFR2 R22 exemplary ribozyme construct SEQ ID NO:114.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
QS Synthetic.

XX
PN W020028320-A2.
XX
PD 07-NOV-2002.
XX
XX 01-MAY-2002; 2002MO-US013679.
XX
PR 01-MAY-2001; 2001US-00847601.
XX
XX (UYFL) UNIV FLORIDA.
PA
XX Lewin AS, Shaw LC, Grant MB;
XX
DR WPI; 2003-111880/10.
XX
PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
XX
XX Claim 1; Page 81; 115pp; English.
XX
CC The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, INOS,
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC dysfunction, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC local vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 34 BP; 10 A; 7 C; 9 G; 0 T; 8 U; 0 Other;
XX
Query Match 76.5%; Score 26; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 AACUGAUGAGCCGUCGCGGGAAC 30
DB 5 AACUGAUGAGCCGUCGCGGGAAC 30
XX
RESULT 7
AB272864
ID AB272864 standard; RNA; 34 BP.
XX
AC AB272864;
XX
DT 09-APR-2003 (first entry)
XX
DE Alpha V R22 exemplary ribozyme construct SEQ ID NO:99.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

AB272855
ID AB272855 standard; RNA; 34 BP.
XX
AC AB272855;
XX
DT 09-APR-2003 (first entry)
XX
DE A2B R21 exemplary ribozyme construct SEQ ID NO:90.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KM ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KM blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
XX
PN WO200288320-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US013679.
XX
PR 01-MAY-2001; 2001US-00847601.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Lewin AS, Shaw LC, Grant MB;
XX
XX WPI; 2003-111880/10.
XX
DR
XX
XX A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
XX Claim 1; Page 80; 115pp; English.
XX
XX The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, iNOS,
CC RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 34 BP; 10 A; 8 C; 10 G; 0 T; 6 U; 0 Other;
SQ
Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db
6 ACUGAUGAGCCGUTCGCGCGAAAC 30
|||||
RESULT 10
AB272862
ID AB272862 standard; RNA; 34 BP.
XX
AC AB272862;
XX
DT 09-APR-2003 (first entry)
XX
DE Alpha 1 R22 exemplary ribozyme construct SEQ ID NO:97.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KM ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KM blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
XX
PN WO200288320-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US013679.
XX
PR 01-MAY-2001; 2001US-00847601.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Lewin AS, Shaw LC, Grant MB;
XX
XX WPI; 2003-111880/10.
XX
DR
XX
XX A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
XX Claim 1; Page 80; 115pp; English.
XX
XX The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, iNOS,
CC RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 34 BP; 7 A; 10 C; 9 G; 0 T; 8 U; 0 Other;
SQ

Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 6 ACTGATGAGCGCGGCGGAAC 30
6 ACUGATGAGCGCGGCGGAAC 30

RESULT 11

ABZ72856
ID ABZ72856 standard; RNA; 34 BP.

AC ABZ72856;

DT 09-APR-2003 (first entry)

XX A2B R22 exemplary ribozyme construct SEQ ID NO:91.

XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
XX ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
XX diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
XX blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

OS Synthetic.

XX MO200288320-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002MO-US013679.

XX 01-MAY-2001; 2001US-00847601.

XX (UYFL) UNIV FLORIDA.

XX Lewin AS, Shaw LC, Grant MB;

XX WPI; 2003-111880/10.

XX A recombinant adeno-associated virus-vectored ribozyme composition,
XX useful for treating a disease or dysfunction of the mammalian eye e.g.
XX retinal disease, e.g. diabetic retinopathy or age-related macular
XX degeneration.

XX Claim 1; Page 80; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, INOS,
XX RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector
XX comprising the ribozyme or the polynucleotide. Also described is a method
XX for decreasing the amount of mRNA encoding a selected polypeptide in a
XX retinal cell of a mammalian eye, comprising providing to the eye the
XX composition described above, and for a time effective to specifically
XX cleave the mRNA in the cell. (I) has ophthalmological activity, and can
XX be used in gene therapy. (I) can be used for treating a disease or
XX dysfunction of the mammalian eye, such as a retinal disease or retinal
XX degeneration. (I) is also useful for manufacturing a medicament for
XX treating the diseases mentioned above, including autosomal dominant
XX retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
XX for treating, decreasing the severity, or ameliorating the symptoms of a
XX pathological condition, e.g. atrophic or pigmented lesions of the eye,
XX blindness, a reduction in central or peripheral vision, or a reduction in

CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention
XX

XX Sequence 34 BP; 9 A; 8 C; 11 G; 0 T; 6 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 6 ACTGATGAGCGCGGCGGAAC 30
6 ACUGATGAGCGCGGCGGAAC 30

RESULT 12

ABZ72870
ID ABZ72870 standard; RNA; 34 BP.

AC ABZ72870;

DT 09-APR-2003 (first entry)

XX VEGFR1 R21 exemplary ribozyme construct SEQ ID NO:111.

XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
XX ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
XX diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
XX blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

OS Synthetic.

XX MO200288320-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002MO-US013679.

XX 01-MAY-2001; 2001US-00847601.

XX (UYFL) UNIV FLORIDA.

XX Lewin AS, Shaw LC, Grant MB;

XX WPI; 2003-111880/10.

XX A recombinant adeno-associated virus-vectored ribozyme composition,
XX useful for treating a disease or dysfunction of the mammalian eye e.g.
XX retinal disease, e.g. diabetic retinopathy or age-related macular
XX degeneration.

XX Claim 1; Page 81; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, INOS,
XX RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector
XX comprising the ribozyme or the polynucleotide. Also described is a method
XX for decreasing the amount of mRNA encoding a selected polypeptide in a
XX retinal cell of a mammalian eye, comprising providing to the eye the
XX composition described above, and for a time effective to specifically
XX cleave the mRNA in the cell. (I) has ophthalmological activity, and can
XX be used in gene therapy. (I) can be used for treating a disease or
XX dysfunction of the mammalian eye, such as a retinal disease or retinal
XX degeneration. (I) is also useful for manufacturing a medicament for

CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (1) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention

XX Sequence 34 BP; 8 A; 12 C; 8 G; 0 T; 6 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACUGAUGAGCCGUGCGCGGAAC 30
Db 6 ACUGAUGAGCCGUGCGCGGAAC 30

RESULT 13
ABZ72860
ID ABZ72860 standard; RNA; 34 BP.

XX ABZ72860;

XX 09-APR-2003 (first entry)

DE Alpha 5 R22 exemplary ribozyme construct SEQ ID NO:95.

KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX

OS Synthetic.

PN WO20028320-A2.

XX 07-NOV-2002.

PF 01-MAY-2002; 2002WO-US013679.

PR 01-MAY-2001; 2001US-00847601.

XX (UYFL) UNIV FLORIDA.

PI Lewin AS, Shaw LC, Grant MB;

DR WPI; 2003-111880/10.

PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.

XX Claim 1; Page 80; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (1). (1) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, inos,
XX RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector
XX comprising the ribozyme or the polynucleotide; or (e) a host cell
XX for decreasing the amount of mRNA encoding a selected polypeptide in a
XX retinal cell of a mammalian eye, comprising providing to the eye the
XX composition described above, and for a time effective to specifically

CC cleave the mRNA in the cell. (1) has ophthalmological activity, and can
CC be used in gene therapy. (1) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC dysfunction. (diabetic) retinopathy, or (age-related) macular
CC degeneration. (1) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (1) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention

XX Sequence 34 BP; 8 A; 8 C; 13 G; 0 T; 5 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACUGAUGAGCCGUGCGCGGAAC 30
Db 6 ACUGAUGAGCCGUGCGCGGAAC 30

RESULT 14
ABZ72861
ID ABZ72861 standard; RNA; 34 BP.

XX ABZ72861;

XX 09-APR-2003 (first entry)

DE Alpha 1 R21 exemplary ribozyme construct SEQ ID NO:96.

KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX

OS Synthetic.

PN WO20028320-A2.

XX 07-NOV-2002.

PF 01-MAY-2002; 2002WO-US013679.

PR 01-MAY-2001; 2001US-00847601.

XX (UYFL) UNIV FLORIDA.

PI Lewin AS, Shaw LC, Grant MB;

DR WPI; 2003-111880/10.

PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.

XX Claim 1; Page 80; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (1). (1) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, inos,
XX RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector

comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (1) has ophthalmological activity, and can be used in gene therapy. (1) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal dysfunction. (diabetic) retinopathy, or (age-related) macular degeneration. (1) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (1) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. AB272763 to AB272953 represent sequences used in the exemplification of the present invention

Sequence 34 BP; 8 A; 9 C; 8 G; 0 T; 9 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.00058; Mismatches 0; Gaps 0;

Matches 25; Conservative 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGTCGCGGCAAC 30
 ||:|||||:|||||
 DB 6 ACUGAUGAGCCGTCGCGGCAAC 30

RESULT 15

AAC8594 AAC8594 standard; DNA; 44 BP.

XX AAC8594;

XX 02-MAR-2001 (first entry)

XX Oligonucleotide #1 used to clone ribozyme SOD-1.295.

XX Ribozyme; retinal degradation; retinal disease; learning; memory;

KW amyloidotic lateral sclerosis; tumour suppression; ss.

XX Mus sp.

XX WO200066780-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US011509.

XX 30-APR-1999; 99US-0131942P.

XX (UYFL) UNIV FLORIDA.

XX Lewin AS, Muzyczka N, Hauswirth WW, Teschendorf C, Burger C;

XX WPI; 2000-687548/67.

XX Novel methods for identifying genes with selected functions comprising contacting genes with a library of ribozymes, useful for identifying PT genes involved in, e.g. retinal disease, learning or memory and tumor suppression.

XX Example 7; Fig 36; 11pp; English.

XX The present invention relates to a method for identifying a gene with a CC selected function comprising contacting genes with a library of ribozymes CC and identifying at least 1 ribozyme that alters the selected function of CC the gene. The present sequence is an oligonucleotide used in the present CC invention. The methods (and ribozymes) are useful for identifying novel CC genes involved in retinal degradation, retinal disease, learning or CC memory, amyloidotic lateral sclerosis or tumour suppression, and for CC producing non-human animal models of diseases

XX Sequence 44 BP; 13 A; 11 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 73.5%; Score 25; DB 3; Length 44;

Best Local Similarity 84.0%; Pred. No. 0.00057; Mismatches 0; Gaps 0;

Matches 21; Conservative 4; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGTCGCGGCAAC 30
 ||:|||||:|||||
 DB 11 ACTGATGAGCCGTCGCGGCAAC 35

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2006, 09:50:18 ; Search time 716 Seconds
(without alignments)
583.491 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size: 1

Total number of hits satisfying chosen parameters: 37781012

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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16: /BMC_Celerra_SIDS3/prodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	US-09-847-601B-100	Sequence 100, App
2	27	79.4	32	US-09-847-601B-101	Sequence 101, App
3	27	79.4	34	US-09-847-601B-98	Sequence 98, App
4	26	76.5	34	US-09-847-601B-92	Sequence 92, App
5	26	76.5	34	US-09-847-601B-93	Sequence 93, App
6	26	76.5	34	US-09-847-601B-99	Sequence 99, App
7	25	73.5	34	US-09-847-601B-90	Sequence 90, App
8	25	73.5	34	US-09-847-601B-91	Sequence 91, App
9	25	73.5	34	US-09-847-601B-95	Sequence 95, App
10	25	73.5	34	US-09-847-601B-96	Sequence 96, App
11	25	73.5	34	US-09-847-601B-97	Sequence 97, App
12	19	55.9	34	US-09-847-601B-94	Sequence 94, App
13	16	47.1	463	US-10-437-963-3252	Sequence 3252, App
14	16	47.1	1845	US-10-156-761-3619	Sequence 3619, App
15	16	47.1	5335	US-10-437-963-18859	Sequence 18859, App
16	16	47.1	6919	US-11-097-143-5630	Sequence 5630, App
17	16	47.1	9025608	US-10-156-761-1	Sequence 1, App

C 18	15	44.1	200	3	US-09-960-352-4463	Sequence 4463, App
C 19	15	44.1	250	3	US-09-864-761-31920	Sequence 31920, App
C 20	15	44.1	307	8	US-10-437-963-99234	Sequence 99234, App
C 21	15	44.1	343	9	US-10-425-115-36422	Sequence 36422, App
C 22	15	44.1	379	3	US-09-867-701-4078	Sequence 4078, App
C 23	15	44.1	389	4	US-09-925-065A-554407	Sequence 554407, App
C 24	15	44.1	522	8	US-09-925-065A-554407	Sequence 554407, App
C 25	15	44.1	522	8	US-10-282-122A-11370	Sequence 11370, App
C 26	15	44.1	573	3	US-09-864-761-15387	Sequence 15387, App
C 27	15	44.1	575	4	US-09-925-065A-637541	Sequence 637541, App
C 28	15	44.1	575	4	US-09-925-065A-637542	Sequence 637542, App
C 29	15	44.1	575	5	US-09-925-065A-637541	Sequence 637541, App
C 30	15	44.1	575	5	US-09-925-065A-637542	Sequence 637542, App
C 31	15	44.1	634	7	US-10-094-097B-106	Sequence 106, App
C 32	15	44.1	714	8	US-10-282-122A-14226	Sequence 14226, App
C 33	15	44.1	810	7	US-10-156-761-2123	Sequence 2123, App
C 34	15	44.1	852	8	US-10-282-122A-26469	Sequence 26469, App
C 35	15	44.1	873	8	US-10-282-122A-12733	Sequence 12733, App
C 36	15	44.1	939	7	US-10-156-761-4428	Sequence 4428, App
C 37	15	44.1	954	9	US-10-493-462-40	Sequence 462, App
C 38	15	44.1	957	8	US-10-282-122A-28269	Sequence 28269, App
C 39	15	44.1	974	6	US-10-198-846-13796	Sequence 13796, App
C 40	15	44.1	1155	6	US-10-309-515-9	Sequence 9, App
C 41	15	44.1	1155	7	US-10-126-764-9	Sequence 9, App
C 42	15	44.1	1401	8	US-10-181-906-5	Sequence 5, App
C 43	15	44.1	1413	3	US-09-815-242-6074	Sequence 6074, App
C 44	15	44.1	1413	7	US-10-369-493-24531	Sequence 24531, App
C 45	15	44.1	1413	8	US-10-282-122A-20379	Sequence 20379, App

ALIGNMENTS

RESULT 1
US-09-847-601B-100
Sequence 100, Application US/09847601B
Publication No. US20050096282A1
GENERAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAM, LYNN C.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
FILE REFERENCE: 4300, 014100
CURRENT APPLICATION NUMBER: US/09/847, 601B
CURRENT FILING DATE: 2001-05-01, 601B
PRIOR APPLICATION NUMBER: 09/063,667
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 100
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-100
Query Match 100.0%; Score 34; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 UGCAACUGAUGAGCGGUCGCGGAAACGAAG 34
Db 1 UGCAACUGAUGAGCGGUCGCGGAAACGAAG 34
-RESULT 2
US-09-847-601B-101

Sequence 101, Application US/09847601B
Publication No. US20050096282A1
GENERAL INFORMATION:
APPLICANT: SHAW, ALFRED S.
APPLICANT: LEWIN, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
METHODS FOR THE TREATMENT OF RETINAL DISEASES
FILE REFERENCE: 4300.014100
CURRENT FILING DATE: 2001-05-01
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1998-04-21
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 101
LENGTH: 32
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-101

Query Match 79.4%; Score 27; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 AACUGAUGAGCCGUCGCGGCGGAAACG 31
Db 3 AACUGAUGAGCCGUCGCGGCGGAAACG 29

RESULT 3
US-09-847-601B-98
Sequence 98, Application US/09847601B
Publication No. US20050096282A1
GENERAL INFORMATION:
APPLICANT: SHAW, ALFRED S.
APPLICANT: LEWIN, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
METHODS FOR THE TREATMENT OF RETINAL DISEASES
FILE REFERENCE: 4300.014100
CURRENT FILING DATE: 2001-05-01
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1998-04-21
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 98
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-98

Query Match 79.4%; Score 27; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 AACUGAUGAGCCGUCGCGGCGGAAACG 31
Db 5 AACUGAUGAGCCGUCGCGGCGGAAACG 31

RESULT 4
US-09-847-601B-92
Sequence 92, Application US/09847601B
Publication No. US20050096282A1
GENERAL INFORMATION:
APPLICANT: SHAW, ALFRED S.
APPLICANT: LEWIN, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
METHODS FOR THE TREATMENT OF RETINAL DISEASES
FILE REFERENCE: 4300.014100
CURRENT FILING DATE: 2001-05-01
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1998-04-21
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 92
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-92

Query Match 76.5%; Score 26; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 AACUGAUGAGCCGUCGCGGCGGAAAC 30
Db 5 AACUGAUGAGCCGUCGCGGCGGAAAC 30

RESULT 5
US-09-847-601B-93
Sequence 93, Application US/09847601B
Publication No. US20050096282A1
GENERAL INFORMATION:
APPLICANT: SHAW, ALFRED S.
APPLICANT: LEWIN, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
METHODS FOR THE TREATMENT OF RETINAL DISEASES
FILE REFERENCE: 4300.014100
CURRENT FILING DATE: 2001-05-01
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1998-04-21
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1997-05-09
PRIORITY FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-93

Query Match 76.5%; Score 26; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 AACUGAUGAGCCGUCGCGGCGGAAAC 30

Db 5 AACUGAGAGCCGUCGCGGGAAC 30

RESULT 6
US-09-847-601B-99

Sequence 99, Application US/09847601B
Publication No. US20050096282A1
GENERAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
FILE REFERENCE: 4300.014100
CURRENT APPLICATION NUMBER: US/09/847,601B
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 09/063,667
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 99
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-99

Query Match 76.5%; Score 26; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAGAGCCGUCGCGGGAAC 30
Db 5 AACUGAGAGCCGUCGCGGGAAC 30

RESULT 7
US-09-847-601B-90

Sequence 90, Application US/09847601B
Publication No. US20050096282A1
GENERAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
FILE REFERENCE: 4300.014100
CURRENT APPLICATION NUMBER: US/09/847,601B
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 09/063,667
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 90
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-90

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAGAGCCGUCGCGGGAAC 30
Db 6 ACUGAGAGCCGUCGCGGGAAC 30

RESULT 8
US-09-847-601B-91

Sequence 91, Application US/09847601B
Publication No. US20050096282A1
GENERAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
FILE REFERENCE: 4300.014100
CURRENT APPLICATION NUMBER: US/09/847,601B
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 09/063,667
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 91
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-91

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAGAGCCGUCGCGGGAAC 30
Db 6 ACUGAGAGCCGUCGCGGGAAC 30

RESULT 9
US-09-847-601B-95

Sequence 95, Application US/09847601B
Publication No. US20050096282A1
GENERAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
FILE REFERENCE: 4300.014100
CURRENT APPLICATION NUMBER: US/09/847,601B
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 09/063,667
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 95
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-95

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
|||||
DB 6 ACUGAUGAGCCGUCGCGCGGAAC 30

RESULT 10

US-09-847-601B-96
; Sequence 96, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-96

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
|||||
DB 6 ACUGAUGAGCCGUCGCGCGGAAC 30

RESULT 11

US-09-847-601B-97
; Sequence 97, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial

FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-97

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
|||||
DB 6 ACUGAUGAGCCGUCGCGCGGAAC 30

RESULT 12

US-09-847-601B-94
; Sequence 94, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-94

Query Match 55.9%; Score 19; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCGGUCGCGCGGAAC 30
|||||
DB 12 GAGCGGUCGCGCGGAAC 30

RESULT 13

US-10-437-963-3252/c
; Sequence 3252, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 3252
; LENGTH: 463
; TYPE: DNA

ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_102953C.1
US-10-437-963-3252

Query Match 47.1%; Score 16; DB 8; Length 463;
Best Local Similarity 81.2%; Pred. No. 22;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGCAACUGAUGAGCC 16
DB 221 TGCMACTGATGAGCC 206

RESULT 14

US-10-156-761-3619
Sequence 3619, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3619
LENGTH: 1845
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1845)
US-10-156-761-3619

Query Match 47.1%; Score 16; DB 7; Length 1845;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCCGUGCGGCGGA 27
DB 1633 GAGCCGTTGCGGCGGA 1648

RESULT 15

US-10-437-963-18859
Sequence 18859, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 18859

LENGTH: 5335
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(5335)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_24377C.1
US-10-437-963-18859

Query Match 47.1%; Score 16; DB 8; Length 5335;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCCGUGCGGCGGA 27
DB 352 GAGCCGTTGCGGCGGA 367

Search completed: August 28, 2006, 10:41:09
Job time : 718 secs

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OM nucleic - nucleic search, using sw model

Run on: August 28, 2006, 09:54:05 / Search time 780 Seconds
(without alignments)
71.045 Million cell updates/sec

Title: US-09-847-601B-100

Perfect score: 34
Sequence: 1 ugcaaaugaugagcgucgagcggaacgaag 34

Scoring table: OLIGO_NTC
Gapop 60.0, Gapext 60.0

Searched: 2239192 seqs, 814926892 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4478184

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Published Applications NA New:

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2: /EMC Celerra SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq:
3: /EMC Celerra SIDS3/prodata/1/pubpna/US07_NEW_PUB.seq:
4: /EMC Celerra SIDS3/prodata/1/pubpna/US08_NEW_PUB.seq:
5: /EMC Celerra SIDS3/prodata/1/pubpna/PCT_NEW_PUB.seq:
6: /EMC Celerra SIDS3/prodata/1/pubpna/US10_NEW_PUB.seq:
7: /EMC Celerra SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq:
8: /EMC Celerra SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq1:
9: /EMC Celerra SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq2:
10: /EMC Celerra SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	47.1	1809	US-10-449-902-27861	Sequence 27861, A
2	15	44.1	1084	US-11-266-748A-184169	Sequence 184169, A
3	15	44.1	1084	US-11-266-748A-191642	Sequence 191642, A
4	15	44.1	1155	US-11-266-748A-25135	Sequence 25135, A
5	15	44.1	1243	US-10-449-902-20318	Sequence 20318, A
6	15	44.1	1249	US-10-449-902-4455	Sequence 4455, Ap
7	15	44.1	1342	US-11-266-748A-312890	Sequence 312890, A
8	15	44.1	1342	US-11-266-748A-312407	Sequence 312407, A
9	15	44.1	1551	US-10-449-902-20725	Sequence 20725, A
10	15	44.1	1773	US-11-266-748A-184170	Sequence 184170, A
11	15	44.1	2253	US-11-266-748A-191643	Sequence 191643, A
12	15	44.1	2253	US-11-266-748A-191643	Sequence 191643, A
13	15	44.1	2752	US-11-248-718-73	Sequence 73, Appl
14	15	44.1	2752	US-11-248-718-73	Sequence 73, Appl
15	15	44.1	2775	US-11-266-748A-29125	Sequence 29125, A
16	15	44.1	3309	US-10-449-902-15931	Sequence 15931, A
17	15	44.1	3389	US-10-449-902-22857	Sequence 22857, A
18	15	44.1	3389	US-10-449-902-22857	Sequence 22857, A
19	15	44.1	3946	US-11-266-748A-44547	Sequence 44547, A
20	15	41.2	611	US-11-266-748A-362168	Sequence 362168, A
21	15	41.2	611	US-11-266-748A-44547	Sequence 44547, A
22	15	41.2	620	US-11-266-748A-6564	Sequence 6564, Ap
23	15	41.2	642	US-11-266-748A-98682	Sequence 98682, A
			642	US-11-266-748A-151493	Sequence 151493, A

C 24	14	41.2	777	8	US-11-266-748A-174235	Sequence 174235, A
C 25	14	41.2	777	8	US-11-266-748A-190325	Sequence 190325, A
C 26	14	41.2	795	8	US-11-056-355B-78299	Sequence 78299, A
C 27	14	41.2	820	8	US-11-266-748A-189268	Sequence 189268, A
C 28	14	41.2	918	8	US-11-266-748A-352337	Sequence 352337, A
C 29	14	41.2	918	8	US-11-266-748A-435716	Sequence 435716, A
C 30	14	41.2	1169	6	US-10-449-902-11462	Sequence 11462, A
C 31	14	41.2	1211	6	US-10-520-999-5	Sequence 5, Appl
C 32	14	41.2	1229	6	US-10-520-999-4	Sequence 4, Appl
C 33	14	41.2	1253	6	US-10-520-999-1	Sequence 1, Appl
C 34	14	41.2	1280	6	US-10-520-999-3	Sequence 3, Appl
C 35	14	41.2	1607	6	US-10-520-999-2	Sequence 2, Appl
C 36	14	41.2	1812	6	US-10-471-571A-4927	Sequence 4927, Ap
C 37	14	41.2	1937	8	US-11-216-545-3254	Sequence 3254, Ap
C 38	14	41.2	2031	9	US-11-218-305-10001	Sequence 10001, A
C 39	14	41.2	2043	6	US-10-520-999-6	Sequence 6, Appl
C 40	14	41.2	2638	9	US-11-218-305-13290	Sequence 13290, A
C 41	14	41.2	3134	9	US-11-218-305-10002	Sequence 10002, A
C 42	14	41.2	3786	6	US-10-473-173-28	Sequence 28, Appl
C 43	14	41.2	4009	8	US-11-266-748A-24493	Sequence 24493, A
C 44	14	41.2	5514	8	US-11-266-748A-30117	Sequence 30117, A
C 45	14	41.2	5964	8	US-11-266-748A-28460	Sequence 28460, A

ALIGNMENTS

RESULT 1
US-10-449-902-27861
Sequence 27861, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: Foundation for Advancement of International Science.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27861
LENGTH: 1809
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK103403
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-27861

Query Match 47.1%; Score 16; DB 6; Length 1809;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCCGUCGCGCGA 27
DB 537 GAGCCGTCGCGCGA 552

RESULT 2
US-11-266-748A-184169
Sequence 184169, Application US/11266748A
Publication No. US20060134653A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Kari
TITLE OF INVENTION: Transcriptome Microarray Technology and

```

; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 184169
; LENGTH: 1084
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-184169
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Query Match      44.1%; Score 15; DB 8; Length 1084;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Oy      6 ACUGAUGAGCCGUTC 20
Db      736 ACTGATGAGCCGTTTC 750
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RESULT 3
US-11-266-748A-191642
; Sequence 191642, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harrin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191642
; LENGTH: 1084
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-191642
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```
Query Match      44.1%; Score 15; DB 8; Length 1084;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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```
Oy      6 ACUGAUGAGCCGUTC 20
Db      736 ACTGATGAGCCGTTTC 750
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RESULT 4
US-11-266-748A-25135
; Sequence 25135, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harrin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25135
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-25135
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Query Match      44.1%; Score 15; DB 8; Length 1155;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Oy      6 ACUGAUGAGCCGUTC 20
Db      538 ACTGATGAGCCGTTTC 552
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RESULT 5
US-10-449-902-20318
; Sequence 20318, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
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Query Match	44.1%	Score 15;	DB 8;	Length 1342;
Best Local Similarity	73.3%	Pred. No. 11;		
Matches 11;	Conservative 4;	Mismatches 0;	Indels 0;	Gaps 0;
QY	6	ACTGATGACCCGATTC	20	
		: ::		

Db 1025 ACTGATGAGCCGTTT 1039

RESULT 9

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US-10-449-902-20725
Sequence 20725, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ. ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20725
LENGTH: 1551
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK071031
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-20725

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Query Match Similarity	44.1%	Score 15:	DB 6,	Length 1551,
Best Local Similarity	86.7%	Pred. No. 11,		
Matches 13, Conservative	2,	Mismatches	0,	Gaps 0

```

QY      14 GCCGUTCGCGCGGA 28
          |||::|||
Db      291 GCCGTTCCGCGCGGA 305

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RESULT 10
US-11-256-428-61/c
; Sequence 61, Application US/11256428
; Publication No. US20060095987A1
; GENERAL INFORMATION:
; APPLICANT: Niblett, Charles L.
; TITLE OF INVENTION: Methods and Materials for Conferring Resistance to Pests and
; TITLE OF INVENTION: Pathogens of Plants
; FILE REFERENCE: VEN-100
; CURRENT APPLICATION NUMBER: US/11/256,428
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Pratylenchus scribneri rDNA
; US-11-256-428-61

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Query March Similarity	44.1%;	Score 15;	DB 8;	Length 1773;
Best Local Similarity	80.0%;	Pred. No. 11;		
Matches 12; Conservative	3;	Mismatches	0;	Indels 0; Gaps 0;

QY	10	AUGAGCCG	UUCGCGG	24
		:	: :	
Db	72	ATGAGCCG	TTGCGGG	58

RESULT 11
US-11-266-748A-184170
Sequence 184170, Application US/11266748A

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Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Har'kin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 184170
LENGTH: 2253
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2038)..(2011)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-184170

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Query Match	44.1%	Score 15;	DB 8;	Length 2255;
Best Local Similarity	73.3%;	Pred. No. 11;		
Matches 11; Conservative	4;	Mismatches 0;	Indels 0;	Gaps 0;

QY 6 ACUGAUGAGCCCGUUC 20
||:|||||:|
Db 796 ACTGATGAGCCGTTTC 810

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RESULT 12
US-11-266-748A-191663
Sequence 191643, Application US/11266748A
Publication NO. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcptome Microarray Technology and
TITLE OF INVENTION: Method of Using the Same
FILE REFERENCE: 55815-0102 (315189)
CURRENT APPLICATION NUMBER: US/11/266, 748A
CURRENT FILING DATE: 2005-11-03
PRIORITY APPLICATION NUMBER: EP 04105479.2
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105482.6
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105483.4
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105507.0
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105485.9
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105484.2
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: US 60/662, 276

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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191643
; LENGTH: 2253
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (2038)..(2071)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-191643
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Query Match          44.1% Score 15; DB 9; Length 2253;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Qy          6 ACUGAUGAGCCGCTTC 20
Db          796 ACTGATGAGCCGCTTC 810
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RESULT 13
US-11-226-554-73
; Sequence 73, Application US/11226554
; Publication No. US20060147373A1
; GENERAL INFORMATION:
; APPLICANT: Caltns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hallan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1
; CURRENT APPLICATION NUMBER: US/11/226,554
; PRIOR FILING DATE: 2005-09-13/177,488
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 73
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-226-554-73
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Query Match          44.1% Score 15; DB 9; Length 2752;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Qy          6 ACUGAUGAGCCGCTTC 20
Db          746 ACTGATGAGCCGCTTC 760
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RESULT 14
US-11-248-718-73
; Sequence 73, Application US/11248718
; Publication No. US20060160997A1
; GENERAL INFORMATION:
; APPLICANT: Caltns, Belinda
; APPLICANT: Chen, Ruihuan
```

```

; APPLICANT: Frantz, Gretchen
; APPLICANT: Hallan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1 US
; CURRENT APPLICATION NUMBER: US/11/248,718
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/300,880
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/304,813
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/312,312
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 60/314,280
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/339,227
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/336,827
; PRIOR FILING DATE: 2001-11-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 73
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-248-718-73

Query Match          44.1% Score 15; DB 9; Length 2752;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Qy          6 ACUGAUGAGCCGCTTC 20
Db          746 ACTGATGAGCCGCTTC 760
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RESULT 15
US-11-266-748A-29125
; Sequence 29125, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29125
; LENGTH: 2775
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-29125

Query Match 44.1%; Score 15; DB 8; Length 2775;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 6 ACUGAUGAGCCGUC 20
||:|||||:|
Db 804 ACTGATGAGCCGTC 818

Search completed: August 28, 2006, 10:07:13
Job time : 781 secs

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OW nucleic - nucleic search, using sw model

Run on: August 28, 2006, 09:45:17 ; Search time 2332 Seconds
(without alignments)
815.290 Million cell updates/sec

Title: US-09-847-601B-100

Perfect score: 34
Sequence: 1 ucgaacugaugagcgucgcgcgaacgaag 34

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size: 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

EST: *
1: gb_est1: *
2: gb_est3: *
3: gb_est4: *
4: gb_est5: *
5: gb_est6: *
6: gb_hic: *
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8: gb_est7: *
9: gb_est8: *
10: gb_est9: *
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12: gb_g882: *
13: gb_g883: *
14: gb_g884: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	18	52.9	470	1	AV681631
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4	18	52.9	592	13	CZ820348 OC_Ba019
5	18	52.9	660	13	CZ804464 OC_Ba017
6	18	52.9	910	13	CZ878583 OC_Ba028
7	17	50.0	591	14	DU808944 OG_Aba009
8	17	50.0	666	13	CL554761 OB_Ba000
9	17	50.0	738	14	DU660702 OG_Aba006
10	17	50.0	763	14	DX010184 OG_Aba011
11	17	50.0	795	14	DX290906 OR_Aba019
12	17	50.0	904	13	CM785911 SP_Ba001
13	17	50.0	955	14	DU759063 ASNG2280.
14	17	50.0	1299	12	BZ692135 SP_Ba001
15	16	47.1	359	4	BM686835
16	16	47.1	367	4	BM805921
17	16	47.1	456	10	N71828
18	16	47.1	515	11	AZ928987
19	16	47.1	518	13	CZ727431

C 20	16	47.1	521	11	BH844497	BH844497 TC3-54H5.
C 21	16	47.1	522	8	CV095014	CV095014 FAMU USDA
C 22	16	47.1	588	4	BX333850	BX333850 BX333850
C 23	16	47.1	657	13	CZ178899	CZ178899 MIRA-BA04
C 24	16	47.1	730	14	AG325093	AG325093 Mus muscu
C 25	16	47.1	779	5	CF208340	CF208340 CAB20003
C 26	16	47.1	794	5	CF287058	CF287058 AGNCOURT
C 27	16	47.1	811	14	CNS04Q59	AL302994 Tetradon
C 28	16	47.1	839	8	CV214664	CV214664 EST74374
C 29	16	47.1	874	10	DV006952	DV006952 CNB243-H0
C 30	16	47.1	907	8	CO023557	CO023557 EST819650
C 31	16	47.1	946	7	AM155158	AM155158 mg1e0002G
C 32	16	47.1	1083	13	CM929167	CM929167 EDCBV35TR
C 33	16	47.1	1120	9	DR140280	DR140280 49191388
C 34	15	44.1	64	7	AM626734	AM626734 SMOVAFCAP
C 35	15	44.1	73	4	CB832373	CB832373 SMDmFCAY
C 36	15	44.1	73	7	AM651879	AM651879 SMD25CANU
C 37	15	44.1	80	8	CO653412	CO653412 081A01D H
C 38	15	44.1	106	1	AA547823	AA547823 MB3D6V1D0
C 39	15	44.1	119	1	AI058040	AI058040 SMMACAC12
C 40	15	44.1	145	2	BM033558	BM033558 kb65e12.Y
C 41	15	44.1	155	14	AJ622806	AJ622806 Drosophi1
C 42	15	44.1	177	4	CB856215	CB856215 r149f02.Y
C 43	15	44.1	178	1	AA509306	AA509306 MBAFCX960
C 44	15	44.1	210	2	BI783608	BI783608 kb35e02.Y
C 45	15	44.1	216	7	AM043480	AM043480 SWI4CAK01

ALIGNMENTS

RESULT 1
LOCUS CZ820350
DEFINITION OC_Ba0198H18.r OC_Ba Oryza coarctata genomic clone OC_Ba0198H18
3', genomic survey sequence.
ACCESSION CZ820350
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza coarctata (Porteresia coarctata) -
Oryza coarctata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 311)
Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
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Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0198 row: H column: 18
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends

FEATURES

source
Location/Qualifiers
1..311
/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0198H18"
/isolate="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_lid="OC_Ba"

ORIGIN /note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

Query Match 52.9%; Score 18; DB 13; Length 311;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 11 UGAGCCGUTTCGCGCGAA 28
:|||||:|||||:
Db 225 TGAGCCGTTTCGCGCGAA 242

RESULT 2
AV681631 470 bp mRNA linear EST 16-JAN-2002
LOCUS AV681631 GKB Homo sapiens cDNA clone GKBADJ02 5', mRNA sequence.
DEFINITION AV681631
ACCESSION AV681631
VERSION AV681631.1 GI:10283494
KEYWORDS EST.
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo
1 (bases 1 to 470)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..470
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKBADJ02"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_id="GKB"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match 52.9%; Score 18; DB 1; Length 470;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AAACGATGAGCCGCTCG 21
:|||||:|||||:
Db 273 AAACGATGAGCCGCTCG 230

RESULT 3
CZ802927 579 bp DNA linear GSS 26-JUL-2005
LOCUS CZ802927
DEFINITION OC_Ba0175A06.f OC_Ba Oryza coarctata genomic clone OC_Ba0175A06
5', genomic survey sequence.
ACCESSION CZ802927
VERSION CZ802927.1 GI:71242780
KEYWORDS GSS.

SOURCE Oryza coarctata (Porteresia coarctata)
ORGANISM Oryza coarctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 579)
Kim,H., Collura,K., Waisotsaki,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jettly,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
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University of Arizona
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Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0175 row: A column: 06
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends
Location/Qualifiers
1..579
/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0175A06"
/tissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_id="OC_Ba"
/note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 52.9%; Score 18; DB 13; Length 579;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 11 UGAGCCGUTTCGCGCGAA 28
:|||||:|||||:
Db 440 TGAGCCGTTTCGCGCGAA 457

RESULT 4
CZ820348 592 bp DNA linear GSS 26-JUL-2005
LOCUS CZ820348
DEFINITION OC_Ba0198H17.r OC_Ba Oryza coarctata genomic clone OC_Ba0198H17
3', genomic survey sequence.
ACCESSION CZ820348
VERSION CZ820348.1 GI:71260201
KEYWORDS GSS.
SOURCE Oryza coarctata (Porteresia coarctata)
ORGANISM Oryza coarctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 592)
Kim,H., Collura,K., Waisotsaki,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jettly,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
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University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0198 row: H column: 17
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
1. .592
Location/Qualifiers

/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0198H17"
/issue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_11b="OC_Ba"
/note="Vector: PAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 52.9%; Score 18; DB 13; Length 592;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 11 UGAGCGGUCGCGCGGAA 28
:|||||:|||||
Db 253 TGAGCCGTCGCGCGGAA 270

RESULT 5
CZ804464 660 bp DNA linear GSS 26-JUN-2005
LOCUS OC_Ba0177B01.f OC_Ba Oryza coarctata genomic clone OC_Ba0177B01
DEFINITION 5', genomic survey sequence.
ACCESSION CZ804464 GI:71244317
VERSION GSS.
KEYWORDS Oryza coarctata (Porteresia coarctata)
SOURCE Oryza coarctata
ORGANISM Oryza coarctata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 660)
Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
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Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0177 row: B column: 01
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers

FEATURES
source
1. .660
Location/Qualifiers

/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0177B01"
/issue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_11b="OC_Ba"
/note="Vector: PAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 52.9%; Score 18; DB 13; Length 660;

Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 11 UGAGCGGUCGCGCGGAA 28
:|||||:|||||
Db 228 TGAGCCGTCGCGCGGAA 245

RESULT 6
CZ878583 910 bp DNA linear GSS 27-JUN-2005
LOCUS OC_Ba0280C17.f OC_Ba Oryza coarctata genomic clone OC_Ba0280C17
DEFINITION 5', genomic survey sequence.
ACCESSION CZ878583 GI:71354339
VERSION GSS.
KEYWORDS Oryza coarctata (Porteresia coarctata)
SOURCE Oryza coarctata
ORGANISM Oryza coarctata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 910)
Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
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Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0280 row: C column: 17
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers

FEATURES
source
1. .910
Location/Qualifiers

/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0280C17"
/issue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_11b="OC_Ba"
/note="Vector: PAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 52.9%; Score 18; DB 13; Length 910;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 11 UGAGCGGUCGCGCGGAA 28
:|||||:|||||
Db 437 TGAGCCGTCGCGCGGAA 454

RESULT 7
DU808944 591 bp DNA linear GSS 13-DEC-2005
LOCUS OG_ABa0093B05.r OG_ABa Oryza granulata genomic clone OG_ABa0093B05
DEFINITION 3', genomic survey sequence.
ACCESSION DU808944 GI:83604603
VERSION GSS.
KEYWORDS Oryza granulata
SOURCE Oryza granulata
ORGANISM Oryza granulata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ORIGIN

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 591)
SamMiguel,P., Westerman,R., Kim,H., Yu,Y., Misosaki,M., Yost,D.,
Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
OMAP (Oryza Map Alignment Project) - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.199.
Bases 107-697 of the raw sequence (length 1052) were retained after
clipping.
Plate: 0093 row: E column: 05
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
location/Qualifiers
1..591
/organism="Oryza granulata"
/mol_type="genomic DNA"
/db_xref="taxon:110450"
/clone="OG_ABA0093E05"
/issue_type="Young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OG_Aba"
/note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN
Query Match 50.0%; Score 17; DB 14; Length 591;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAGCCGUTCGCGCGCA 28
|||||:|||||
Db 309 GAGCCGTTCCGCGCGCA 325

RESULT 8
LOCUS
DEFINITION
VERSION
KEYWORDS
SOURCE
ORGANISM

CU554761 666 bp DNA linear GSS 14-JUN-2004
OB_Ba0004E01.f OB_Ba Oryza brachyantha genomic clone
CU554761 GI:47632656
GSS.
Oryza brachyantha
Oryza brachyantha
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 666)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
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University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 625 9595
Fax: 520 621 1259
Email: twing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert length: 145000 Std Error: 0.00
Plate: 0004 row: E column: 01

TITLE
JOURNAL
COMMENT

Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
location/Qualifiers
1..666
/organism="Oryza brachyantha"
/mol_type="genomic DNA"
/db_xref="taxon:110450"
/clone="OB_Ba0004E01"
/issue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_lib="OB_Ba"
/note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN
Query Match 50.0%; Score 17; DB 13; Length 666;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAGCCGUTCGCGCGCA 28
|||||:|||||
Db 450 GAGCCGTTCCGCGCGCA 466

RESULT 9
LOCUS
DEFINITION
VERSION
KEYWORDS
SOURCE
ORGANISM

DU660702 738 bp DNA linear GSS 31-OCT-2005
OG_ABA0063J17.r OG_ABA Oryza granulata genomic clone OG_ABA0063J17
3.7 genomic survey sequence.
DU660702 GI:78394844
GSS.
Oryza granulata
Oryza granulata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 738)
SamMiguel,P., Westerman,R., Kim,H., Yu,Y., Misosaki,M., Yost,D.,
Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
OMAP (Oryza Map Alignment Project) - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.199.
Bases 109-846 of the raw sequence (length 938) were retained after
clipping.
Plate: 0063 row: J column: 17
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
location/Qualifiers
1..738
/organism="Oryza granulata"
/mol_type="genomic DNA"
/db_xref="taxon:110450"
/clone="OG_ABA0063J17"
/issue_type="Young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OG_Aba"
/note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN
Query Match 50.0%; Score 17; DB 14; Length 738;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

TITLE
JOURNAL
COMMENT

Qy 12 GAGCCGTCGCGCGCAA 28
|||||:|||||
Db 588 GAGCCGTCGCGCGCAA 604

RESULT 10
DX010184 763 bp DNA linear GSS 05-JAN-2006
LOCUS OG_Aba0110K10.f OG_Aba Oryza granulata genomic clone OG_Aba0110K10
DEFINITION 5', genomic survey sequence.
ACCESSION DX010184 GI:84416351
VERSION DX010184.1 GI:84416351
KEYWORDS GSS.
SOURCE Oryza granulata
ORGANISM Oryza granulata
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Eriarthroidae; Oryzaceae; Oryza.

REFERENCE
AUTHORS SamMiguel,P., Westerman,R., Kim,H., Yu,Y., Misotski,M., Yost,D.,
1 (bases 1 to 763)
Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
TITLE OMAP (Oryza Map Alignment Project) - Purdue University
JOURNAL Unpublished (2004)
COMMENT Contact: Scott A. Jackson
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Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu

FEATURES
source
1..763 location/Qualifiers
/organism="Oryza granulata"
/mol_type="genomic DNA"
/db_xref="taxon:110450"
/clone="OG_Aba0110K10"
/issue_type="young leaves"
/lab_host="DH10B TI phage resistant"
/clone_1lb="OG_Aba"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 50.0%; Score 17; DB 14; Length 763;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAGCCGTCGCGCGCAA 28
|||||:|||||
Db 315 GAGCCGTCGCGCGCAA 331

RESULT 11
DX290906 795 bp DNA linear GSS 20-JAN-2006
LOCUS OR_Aba0194J18.f OR_Aba Oryza riddlei genomic clone OR_Aba0194J18
DEFINITION 5', genomic survey sequence.
ACCESSION DX290906 GI:85561663
VERSION DX290906.1 GI:85561663
KEYWORDS GSS.
SOURCE Oryza riddlei
ORGANISM Oryza riddlei
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Eriarthroidae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 795)

AUTHORS Kim,H., Collura,K., Misotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
TITLE OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
JOURNAL Unpublished (2005)
COMMENT Contact: Rod A. Wing
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Email: rwing@genome.arizona.edu
Plate: 0194 row: J column: 18
Class: BAC ends.

FEATURES
source
1..795 location/Qualifiers
/organism="Oryza riddlei"
/mol_type="genomic DNA"
/db_xref="taxon:83308"
/clone="OR_Aba0194J18"
/issue_type="leaves"
/lab_host="DH10B"
/clone_1lb="OR_Aba"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 50.0%; Score 17; DB 14; Length 795;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAGCCGTCGCGCGCAA 28
|||||:|||||
Db 238 GAGCCGTCGCGCGCAA 254

RESULT 12
CW785911 904 bp DNA linear GSS 22-NOV-2004
LOCUS SP_Ba0016N09.f SP_Ba Sorghum prolingum genomic clone
DEFINITION SP_Ba0016N09 3', genomic survey sequence.
ACCESSION CW785911 GI:55927805
VERSION CW785911
KEYWORDS GSS.
SOURCE Sorghum prolingum
ORGANISM Sorghum prolingum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE
AUTHORS Bowers,J.E., Arias,M.A., Asher,R., Avise,J.A., Ball,R.T.,
Brewer,G.A., Buss,R.W., Chen,A.H., Edwards,T.M., Eick,J.C.,
Erum,H.B., Goff,V.H., Herrick,K.L., Steele,C.L., Karunakaran,S.,
Lafayette,G.K., Lemke,C., Marler,B.S., Masters,S.L., McMillan,J.M.,
Nelson,L.K., Newsome,G.A., Nwakanma,C.C., Odoh,R.N., Phelps,C.A.,
Rarick,E.A., Rogers,C.J., Ryan,S.P., Slaughter,K.A.,
Soderlund,C.A., Tang,H., Wing,R.A. and Peterson,A.H.
TITLE Comparative physical mapping links conservation of microsatelity to
JOURNAL chromosome structure and recombination in grasses
PUBMED Proc. Natl. Acad. Sci. U.S.A. 102 (37), 13206-13211 (2005)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0016 row: N column: 09
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES

Source

Location/Qualifiers
1. .904
/organism="Sorghum propinquum"
/mol_type="genomic DNA"
/db_xref="taxon:132711"
/clone="SP_Ba0016N09"
/clone_lib="SP_Ba"
/note="Vector: pBelBAC11, Site_1: HindIII, Site_2:
HindIII, Paterson lab BAC library (HindIII)"

ORIGIN

Query Match 50.0%; Score 17; DB 13; Length 904;
Best Local Similarity 76.5%; Pred. No. 47;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAAACUGAUGAGCCGCU 19
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Db 768 CAAACTGATGAGCCGTT 752

RESULT 13 955 bp DNA linear GSS 27-JAN-2006
DUT59063
LOCUS ASNG2280.g2 HF200_10-06-02 uncultured marine microorganism
DEFINITION HF200_10-06-02 genomic clone HF200_082H09, genomic survey
sequence.

ACCESSION DUT59063.1 GI:85768899
VERSION DUT59063
KEYWORDS
SOURCE GSS.

REFERENCE
1 (bases 1 to 955)
uncultured marine microorganism HF200_10-06-02
unclassified sequences; environmental samples.

AUTHORS Delong, E. F., Preston, C. M., Mincer, T., Rich, V., Hallam, S. J.,
Frigaard, N. U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S. W.
and Karl, D. M.

TITLE Comparative genomics reveals ecological trends in stratified
microbial communities in the ocean's interior
Science (2006) In press

JOURNAL Contact: Susan Lucas, Alex Copeland, Sam Pittluck, Alla Lapidus,
Kerrie Barry, Tjiana Glavinadeliro, David Bruce, Paul Richardson
and Edward Delong
US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-2679

EMAIL: pwrichardson@lbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6
um, greater than 0.22 um fraction. Sample Date: 10/6/2002
Coordinates: 22.45 N, 158 W Depth 200 m Temperature: 18.53 C
Salinity: 35.04 psu Oxygen: 198.8 umol/kg
Class: fosmid ends.

FEATURES

Source

Location/Qualifiers
1. .955
/organism="uncultured marine microorganism HF200_10-06-02"
/mol_type="genomic DNA"
/db_xref="taxon:1361147"
/clone="HF200_082H09"
/cell_type="marine picoplankton, less than 1.8 um, greater
than 0.22 um fraction"
/clone_lib="HF200_10-06-02"
/note="Vector: pCC1FOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 200 m
depth on 10/6/2002, Coordinates: 22.45 N, 158 W. Sample
Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 200 m
Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8
umol/kg"

ORIGIN

Query Match 50.0%; Score 17; DB 14; Length 955;
Best Local Similarity 82.4%; Pred. No. 47;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GAUGAGCCGUGUCGCGC 25
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Db 273 GATGAGCCGTTCCGCGC 289

RESULT 14

B2692135/c 1299 bp DNA linear GSS 02-JUL-2003
LOCUS SP_Ba0016N09.r SP_Ba Sorghum propinquum genomic clone
DEFINITION SP_Ba0016N09.3, genomic survey sequence.

ACCESSION B2692135
VERSION B2692135
KEYWORDS
SOURCE GSS.

ORIGIN
Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 1299)

REFERENCE Wing, R., Yu, Y., Kim, H. R., Collura, K., Pries, G., Currie, J.,
Soderlund, C. and Hatfield, J.
Sequencing of Sorghum BAC ends.
http://genome.arizona.edu/stc/sorghum
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288

EMAIL: twing@genome.arizona.edu
PCR Primers
FORWARD: atc agc ggc cgc gat cc
BACKWARD: gta aaa cga cgg cca gtc
Plate: 0016 row: N column: 09
Seq primer: gta aaa cga cgg cca gtc
Class: BAC ends.

FEATURES

Source

Location/Qualifiers
1. .1299
/organism="Sorghum propinquum"
/mol_type="genomic DNA"
/db_xref="taxon:132711"
/clone="SP_Ba0016N09"
/clone_lib="SP_Ba"
/note="Vector: pBelBAC11, Site_1: HindIII, Site_2:
HindIII, Paterson lab BAC library (HindIII)"

ORIGIN

Query Match 50.0%; Score 17; DB 12; Length 1299;
Best Local Similarity 76.5%; Pred. No. 47;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAAACUGAUGAGCCGCU 19
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Db 801 CAAACTGATGAGCCGTT 785

RESULT 15

BW868335 359 bp mRNA linear EST 07-NOV-2005
LOCUS BW868335 Amphioxus Branchiostoma floridae unpublished cDNA library,
neurala whole animal Branchiostoma floridae cDNA clone dfne085101
5', mRNA sequence.

ACCESSION BW868335
VERSION BW868335.1 GI:66483012
KEYWORDS EST.
SOURCE Branchiostoma floridae (Florida lancelet)
ORIGIN Branchiostoma floridae

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 Branchiostoma.
 1 (bases 1 to 359)
 Yu.J., Holland L.Z., Shin-i.T., Kohara.Y., Satou.Y. and Satoh.N.
 Expressed genes in Branchiostoma floridae
 Unpublished (2005)
 Contact: Tadao Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 If you want to have a cDNA clone for this EST or if you have any
 questions, please send an e-mail to Nori Satoh
 (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
 (yutaka@ascidian.zool.kyoto-u.ac.jp).

FEATURES

Source
 1..359
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:7739"
 /clone="bfne085101"
 /tissue_type="whole animal"
 /dev_stage="neurula"
 /clone_lib="Amphioxus Branchiostoma floridae unpublished
 cDNA library, neurula whole animal"

ORIGIN

Query Match 47.1%; Score 16; DB 4; Length 359;
 Best Local Similarity 93.8%; Pred.No. 1.8e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 19 UCGCGCGCAACGAG 34
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 Db 45 TCGCGCGCAACGAG 60

Search completed: August 28, 2006, 10:29:08
 Job time : 2336 secs

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REFERENCE 1 (bases 1 to 32)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 101 14-OCT-2003;
GRI Aerospace; Paris;
FRX;
FEATURES
SOURCE Location/Qualifiers
1. .32
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/mol_type="unassigned RNA"
ORIGIN
Query Match 79.4%; Score 27; DB 2; Length 32;
Best Local Similarity 85.2%; Pred. No. 7.7e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 5 AACUGAUGAGCCGUUCGCGGGAACG 31
Db 3 AACTGATGAGCCGTTCCGCGGGAACG 29
RESULT 3
AR408005 34 bp RNA linear PAT 18-DEC-2003
LOCUS AR408005
DEFINITION Sequence 98 from patent US 6632057.
ACCESSION AR408005
VERSION AR408005.1 GI:40157992
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 98 14-OCT-2003;
GRI Aerospace; Paris;
FRX;
FEATURES
SOURCE Location/Qualifiers
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/mol_type="unassigned RNA"
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Query Match 79.4%; Score 27; DB 2; Length 34;
Best Local Similarity 85.2%; Pred. No. 7.6e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 5 AACUGAUGAGCCGUUCGCGGGAACG 31
Db 5 AACTGATGAGCCGTTCCGCGGGAACG 31
RESULT 4
AR407999 34 bp RNA linear PAT 18-DEC-2003
LOCUS AR407999
DEFINITION Sequence 92 from patent US 6632057.
ACCESSION AR407999
VERSION AR407999.1 GI:40157986
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 92 14-OCT-2003;
GRI Aerospace; Paris;
FRX;
FEATURES
SOURCE Location/Qualifiers
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/mol_type="unassigned RNA"
ORIGIN

Query Match 76.5%; Score 26; DB 2; Length 34;
Best Local Similarity 84.6%; Pred. No. 3.4e-05;
Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 5 AACUGAUGAGCCGUUCGCGGGAAC 30
Db 5 AACTGATGAGCCGTTCCGCGGGAAC 30
RESULT 5
AR408000 34 bp RNA linear PAT 18-DEC-2003
LOCUS AR408000
DEFINITION Sequence 93 from patent US 6632057.
ACCESSION AR408000
VERSION AR408000.1 GI:40157987
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 93 14-OCT-2003;
GRI Aerospace; Paris;
FRX;
FEATURES
SOURCE Location/Qualifiers
1. .34
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/mol_type="unassigned RNA"
ORIGIN
Query Match 76.5%; Score 26; DB 2; Length 34;
Best Local Similarity 84.6%; Pred. No. 3.4e-05;
Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 5 AACUGAUGAGCCGUUCGCGGGAAC 30
Db 5 AACTGATGAGCCGTTCCGCGGGAAC 30
RESULT 6
AR408006 34 bp RNA linear PAT 18-DEC-2003
LOCUS AR408006
DEFINITION Sequence 99 from patent US 6632057.
ACCESSION AR408006
VERSION AR408006.1 GI:40157993
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 99 14-OCT-2003;
GRI Aerospace; Paris;
FRX;
FEATURES
SOURCE Location/Qualifiers
1. .34
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 76.5%; Score 26; DB 2; Length 34;
Best Local Similarity 84.6%; Pred. No. 3.4e-05;
Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 5 AACUGAUGAGCCGUUCGCGGGAAC 30
Db 5 AACTGATGAGCCGTTCCGCGGGAAC 30
RESULT 7

BD263835
LOCUS BD263835 34 bp RNA linear PAT 17-JUL-2003
DEFINITION Adeno-associated virus-delivered ribozyme compositions and methods of use.
ACCESSION BD263835
VERSION BD263835.1 GI:33073603
KEYWORDS JP 2002542805-A/57.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 34)
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods of use
JOURNAL Patent: JP 2002542805-A 57 17-DEC-2002;
COMMENT UNIVERSITY OF FLORIDA
OS Artificial Sequence
PN JP 2002542805-A/57
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615402
PR 30-APR-1999 US 60/131942
PI ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
,CHRISTIAN TESCHENDORF,
PI CORINNA BURGER
PC C12N15/09,A01K67/027,C12N9/00,C12Q1/68,C12N15/00 CC
Description of Artificial Sequence: SYNTHETIC PEPTIDE FH Key
Location/Qualifiers
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/mol_type='genomic RNA'
/db_xref='taxon:32630'

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Query Match 73.5%; Score 25; DB 2; Length 34;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
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6 ACTGATGAGCCGTTCCGCGCGGAAC 30

RESULT 8
AR407997 34 bp RNA linear PAT 18-DEC-2003
LOCUS AR407997
DEFINITION Sequence 90 from patent US 6632057.
ACCESSION AR407997
VERSION AR407997.1 GI:40157984
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 90 14-OCT-2003;
GPI Aerospace; Paris;
FRX; Location/Qualifiers
1..34 /organism='unknown'
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ORIGIN
Query Match 73.5%; Score 25; DB 2; Length 34;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
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6 ACTGATGAGCCGTTCCGCGCGGAAC 30

Db ||:|||||:|||||:
6 ACTGATGAGCCGTTCCGCGCGGAAC 30

RESULT 9
AR407998 34 bp RNA linear PAT 18-DEC-2003
LOCUS AR407998
DEFINITION Sequence 91 from patent US 6632057.
ACCESSION AR407998
VERSION AR407998.1 GI:40157985
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 91 14-OCT-2003;
GPI Aerospace; Paris;
FRX; Location/Qualifiers
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/mol_type='unassigned RNA'

ORIGIN
Query Match 73.5%; Score 25; DB 2; Length 34;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
||:|||||:|||||:
6 ACTGATGAGCCGTTCCGCGCGGAAC 30

RESULT 10
AR408002 34 bp RNA linear PAT 18-DEC-2003
LOCUS AR408002
DEFINITION Sequence 95 from patent US 6632057.
ACCESSION AR408002
VERSION AR408002.1 GI:40157989
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 95 14-OCT-2003;
GPI Aerospace; Paris;
FRX; Location/Qualifiers
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/mol_type='unassigned RNA'

ORIGIN
Query Match 73.5%; Score 25; DB 2; Length 34;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
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6 ACTGATGAGCCGTTCCGCGCGGAAC 30

RESULT 11
AR408003 34 bp RNA linear PAT 18-DEC-2003
LOCUS AR408003
DEFINITION Sequence 96 from patent US 6632057.
ACCESSION AR408003
VERSION AR408003.1 GI:40157990
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 96 14-OCT-2003;
GPI Aerospace; Paris;
FRX;
FEATURES location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 73.5%; Score 25; DB 2; Length 34;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
6 ACTGATGAGCCGTCGCGCGGAAC 30
Db
RESULT 12 34 bp RNA linear PAT 18-DEC-2003
AR408004
LOCUS AR408004
DEFINITION Sequence 97 from patent US 6632057.
ACCESSION AR408004
VERSION AR408004.1 GI:40157991
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 97 14-OCT-2003;
GPI Aerospace; Paris;
FRX;
FEATURES location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 73.5%; Score 25; DB 2; Length 34;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
6 ACTGATGAGCCGTCGCGCGGAAC 30
Db
RESULT 13 34 bp RNA linear PAT 15-DEC-2000
AX048321
LOCUS AX048321
DEFINITION Sequence 57 from Patent WO0066780.
ACCESSION AX048321
VERSION AX048321.1 GI:11877086
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods of use
JOURNAL Patent: WO 0066780-A 97 09-NOV-2000;
University of Florida (US)
FEATURES location/Qualifiers

SOURCE 1..34
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/db_xref="taxon:32630"
/note="SYNTHETIC PEPTIDE"
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Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
6 ACTGATGAGCCGTCGCGCGGAAC 30
Db
RESULT 14 44 bp DNA linear PAT 17-JUL-2003
BD263871
LOCUS BD263871
DEFINITION Adeno-associated virus-delivered ribozyme compositions and methods of use.
ACCESSION BD263871
VERSION BD263871.1 GI:33073639
KEYWORDS JP 2002542805-A/93.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 44)
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods of use
JOURNAL Patent: JP 2002542805-A 93 17-DEC-2002;
UNIVERSITY OF FLORIDA
COMMENT OS Artificial Sequence
PN JP 2002542805-A/93
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615402
PR 30-APR-1999 US 60/131942
PI ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
CHRISTIAN TESCHENDORF,
PI CORINNA BURGER
PC C12N15/09,A01K67/027,C12N9/00,C1201/68,C12N15/00 CC
Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE PH
Key Location/Qualifiers
FT source 1..44
FT location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 73.5%; Score 25; DB 2; Length 44;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
11 ACTGATGAGCCGTCGCGCGGAAC 35
Db
RESULT 15 44 bp DNA linear PAT 15-DEC-2000
AX048357
LOCUS AX048357
DEFINITION Sequence 93 from Patent WO0066780.
ACCESSION AX048357
VERSION AX048357.1 GI:11877122
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods of use
JOURNAL Patent: WO 0066780-A 97 09-NOV-2000;
University of Florida (US)
FEATURES location/Qualifiers

REFERENCE 1
AUTHORS Lewin,A.S., Muzyczka,N., Hauewirth,W.W., Teschendorf,C. and
Burger,C.

TITLE Adeno-associated virus-delivered ribozyme compositions and methods
of use

JOURNAL Patent: WO 0066780-A 93 09-NOV-2000;
University of Florida (US)

FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="SYNTHETIC OLIGONUCLEOTIDE"

ORIGIN

Query Match 73.5%; Score 25; DB 2; Length 44;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACUGAUGAGCCGUGCGCGCGAAG 30
||:|||||:|||||
Db 11 ACTGATGAGCCGTCGCCGCGAAG 35

Search completed: August 28, 2006, 10:26:44
Job time : 2472 secs

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